

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:04:58 ; Search time 4437 Seconds
(without alignments)
11338.802 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	8					Description
	No.	Score	Query Match	Length	ID	
	1	1559.6	75.3	3859	11 AK014464	AK014464 Mus muscu
	2	1554	75.1	3634	11 AK041285	AK041285 Mus muscu
	3	1554	75.1	3877	11 AK033112	AK033112 Mus muscu
	4	1552.4	75.0	4046	11 AK049626	AK049626 Mus muscu
	5	1552.4	75.0	4101	11 AK046175	AK046175 Mus muscu
	6	1530.4	73.9	3805	11 AK082230	AK082230 Mus muscu
	7	1514.2	73.1	3880	11 AK080498	AK080498 Mus muscu
	8	1347.2	65.1	4048	11 AK082317	AK082317 Mus muscu
	9	1068.4	51.6	3147	11 AK079814	AK079814 Mus muscu
	10	991.6	47.9	1114	9 AF150387	AF150387 AF150387
	11	960.8	46.4	2504	11 AK014390	AK014390 Mus muscu
c	12	935.8	45.2	1025	13 BX463709	BX463709 BX463709
	13	819.6	39.6	913	13 BQ949536	BQ949536 AGENCOURT
	14	791.2	38.2	928	13 BU557282	BU557282 AGENCOURT
c	15	787.4	38.0	858	9 AL570757	AL570757 AL570757
	16	763.8	36.9	950	13 BU502697	BU502697 AGENCOURT
	17	751.8	36.3	932	13 BU148788	BU148788 AGENCOURT
c	18	746	36.0	747	12 BQ018588	BQ018588 UI-H-DH1-
	19	740.6	35.8	1059	12 BI084083	BI084083 602869445
c	20	725.2	35.0	956	13 BX433493	BX433493 BX433493
c	21	723.8	35.0	865	12 BI084878	BI084878 602869445
	22	713.8	34.5	761	12 BM016288	BM016288 603642760
	23	705.6	34.1	797	13 BU193314	BU193314 AGENCOURT
	24	690.2	33.3	904	10 BE378929	BE378929 601237528
	25	689.4	33.3	826	13 BU182102	BU182102 AGENCOURT
c	26	681.4	32.9	718	10 BF057767	BF057767 7k53e11.x
	27	679.4	32.8	802	13 BU613719	BU613719 UI-M-EW0-
	28	675.6	32.6	945	13 BQ669630	BQ669630 AGENCOURT
	29	657.8	31.8	684	10 BF338951	BF338951 602036021
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	31	633	30.6	789	10 BF204338	BF204338 601866411
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	34	624	30.1	635	10 BE296749	BE296749 601175134
	35	597	28.8	684	9 AV725513	AV725513 AV725513
	36	595	28.7	623	12 BI828125	BI828125 603075385
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	44	558	27.0	939	10 BF203806	BF203806 601868788
	45	540.8	26.1	624	13 BU708350	BU708350 UI-M-FC0-

ALIGNMENTS

RESULT 1
AK014464
LOCUS AK014464 3859 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04 product:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK014464
VERSION AK014464.1 GI:12852334
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3859)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers
source 1. .3859

CDS

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/db_xref="MGI:1896726"
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/clone="4122401C04"
/tissue_type="head"
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AAITESDKFFINGSNWEGILGLAYAEIARPDSDLPPFFDSL VKQTHI PNI FSLQLCGA
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TTPWNIFPVISLYLMGEVTNQSF RITILPQQYL R PVEDVATSQDDCYKFAVSQSSTGT
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BASE COUNT 873 a 1082 c 1028 g 876 t
ORIGIN

Query Match 75.3%; Score 1559.6; DB 11; Length 3859;
Best Local Similarity 87.5%; Pred. No. 6.2e-193;
Matches 1798; Conservative 0; Mismatches 244; Indels 12; Gaps 8;

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Db 430 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCAC 489

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
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Db 490 GGAACCCATCTCGGCATCCGGCTGCCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 549

Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGAGCTTT 180
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Qy 241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
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Qy 301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
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Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	1330	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCTGGAT	1389
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
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Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
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Db	1570	TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTATCATGGAA	1629

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Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1990		
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Qy	1739	AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA	2168
Qy	1739	CTCTTGCTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC	1798
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Qy	1799	TCC'TTAGACACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC	2227
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Db	2285		
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Db	2344		
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Qy	1979	TTTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT	2038
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Qy 2039 GAATTAAAAAAAAA 2052
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 Db 2460 GAGATAACAAGAA 2473

RESULT 2

AK041285

LOCUS AK041285 3634 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530097B07 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK041285

VERSION AK041285.1 GI:26334342

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3634)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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RESULT 3

AK033112

LOCUS AK033112 3877 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 15 days embryo male testis cDNA, RIKEN full-length

enriched library, clone:8030431G04 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK033112

VERSION AK033112.1 GI:26328834

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

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AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)
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 REFERENCE 5
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 REFERENCE 6 (bases 1 to 3877)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
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 FEATURES Location/Qualifiers
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BASE COUNT 877 a 1090 c 1030 g 880 t
ORIGIN

Query Match 75.1%; Score 1554; DB 11; Length 3877;
Best Local Similarity 87.7%; Pred. No. 3.3e-192;
Matches 1801; Conservative 0; Mismatches 240; Indels 13; Gaps 9;

Qy	1	ATGGCCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGAGTGCTGCCTGCCAC	60
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Db	1110	CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC	1169
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Db	1230	GAAGTGATCATTGTACGTGTGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG	1289
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Db	1290	TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	1349
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Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
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Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTGTACCTTGGACATG	1320
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Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
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Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

- REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
- REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
- REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
- REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
- REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4046)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4046
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:C530008K17"
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 /dev_stage="12 days embryo"

CDS 433..1938
 /note="unnamed protein product; beta-site APP cleaving enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN, 98%, match=3874)
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 /codon_start=1
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 /db_xref="GI:26340362"
 /translation="MAPALHWLLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
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 GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVIVRVEINGQDLKM
 DCKEYNYDKSIVDSGTTNLRLPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAG
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BASE COUNT 951 a 1102 c 1056 g 937 t
ORIGIN

Query Match 75.0%; Score 1552.4; DB 11; Length 4046;
Best Local Similarity 87.6%; Pred. No. 5.2e-192;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Db     433 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCCAG 492

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
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Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGCCGGAGGGGCAGCTTT 180
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Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db 1153 GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT 1212

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Db 1933 AAGTAAGGAGGCCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC 1992

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prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4101)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4101
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/mol_type="mRNA"
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BASE COUNT 964 a 1118 c 1066 g 953 t

ORIGIN

Query Match 75.0%; Score 1552.4; DB 11; Length 4101;
Best Local Similarity 87.6%; Pred. No. 5.1e-192;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
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Db 447 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 506

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Db 507 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 566

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Db 567 CTGAGGCTGCCCCGGGAGACCGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 626

Qy 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db 627 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 686

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Db 687 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA 746

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Qy 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db 807 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 866

Qy 421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db 1227 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 1286

Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACACCCCTTGAACATT	1020
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Qy	1021	TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
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Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
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Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
 Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3805)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.go.jp/>
URL:<http://fantom.gsc.riken.go.jp/>.

FEATURES Location/Qualifiers

source 1. 3805
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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ORIGIN

Query Match 73.9%; Score 1530.4; DB 11; Length 3805;
Best Local Similarity 87.5%; Pred. No. 3.7e-189;
Matches 1800; Conservative 0; Mismatches 241; Indels 15; Gaps 11;

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Db 448 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 507

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Qy	540	GGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTC	599
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Db	1648	AAGGTTTCTATGTCTCTTCGATCGAGCCCCGAAAGCGAATTGGCTTTGCTGTACGCGCTT	1707
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Db	1948	TCAAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTT	2007
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Db	2008	CCCTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACC	2067
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Db	2068	CTCACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATT	2126
Qy	1677	CCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA	1736
Db	2127	ACAGGGCTTGACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAA	2186
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Qy	1917	GAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC	1976
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Qy	1977	TATTTGCTTTAGAGACAGGGACTGTATAAAACAAGCCTAACATTGGTGCAAAGATTGCCTC	2036
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RESULT 7

AK080498

LOCUS AK080498 3880 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730059K08 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK080498

VERSION AK080498.1 GI:26099278

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,

Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3880)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 73.1%; Score 1514.2; DB 11; Length 3880;
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Matches 1797; Conservative 0; Mismatches 243; Indels 17; Gaps 12;

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RESULT 8

AK082317

LOCUS AK082317 4048 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230037E16 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK082317

VERSION AK082317.1 GI:26349644

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 4048)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source Location/Qualifiers

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CDS

451. .1854

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BASE COUNT 952 a 1103 c 1045 g 948 t

ORIGIN

Query Match 65.1%; Score 1347.2; DB 11; Length 4048;

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Matches 1697; Conservative 0; Mismatches 243; Indels 114; Gaps 9;

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Db	811		TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGAA	870
Qy	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	871		CTGGGCACCGACCTGGTGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT	930
Qy	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	931		GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACCTGGGAGGGCATCCTA	990
Qy	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	991		GGGCTGGCCTATGCTGAGATTGCCAGGCCCCGACGACTCTTTGGAGCCCTTCTTTGACTCC	1050
Qy	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	1051		CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC	1110
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	1111		CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC	1170
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	1171		GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT	1230
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	1231		GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG	1290
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCAACCAACCTTCGTTTGCCCAAGAAA	900

Db	1291	-----	1290
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	1291	-----ACGGAGAAGTTCCTGAT	1308
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	1309	GGCTTTTGGCTAGGGGAACAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1368
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1369	TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1428
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1429	ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1488
Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1489	TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA	1548
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1549	GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC	1608
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1609	CATGTGCACGATGAGTTCAGGACGGCAGTGGGAAGGTCCGTTTGTACGGCAGACATG	1668
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
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Db	1729	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG	1788
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1789	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1848
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Db	1849	AAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC	1908
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1909	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1968
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678
Db	1969	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	2027
Qy	1679	AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAACTCTGCTGGCGGGAATA	1738
Db	2028	AGGGCTTGACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA	2087

Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
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Qy 1799 CTTTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
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Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
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 Db 2204 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 2262

Qy 1919 AGAGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
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 Db 2263 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGA--AAGTGAAGTTTGCCA 2319

Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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 Db 2320 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2378

Qy 2039 GAATTAAAAA 2052
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 Db 2379 GAGATAAACAAGAA 2392

RESULT 9

AK079814

LOCUS AK079814 3147 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430076B07 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK079814

VERSION AK079814.1 GI:26098773

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3147)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
source 1. .3147
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A430076B07"
/db_xref="taxon:10090"
/clone="A430076B07"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature 1. .3147
/note="beta-site APP cleaving enzyme (MGD|MGI:1346542,
GB|NM_011792, evidence: BLASTN, 98%, match=3874)"

BASE COUNT 738 a 840 c 791 g 778 t
ORIGIN

Query Match 51.6%; Score 1068.4; DB 11; Length 3147;
Best Local Similarity 86.3%; Pred. No. 2.1e-129;
Matches 1286; Conservative 0; Mismatches 191; Indels 13; Gaps 9;

Qy 565 AGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCC 624
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Db 282 AGGCCCCGACGACTCTTTGGAGCCCTTCTTTGACTCCCTGGTGAAGCAGACCCACATTCCC 341

Qy 625 AACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTG 684
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Db 342 AACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTCCCCCTCAACCAGACCGAGGCACTG 401

Qy 685 GCCTCTGTCTGGAGGGAGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCAGT 744
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Db 402 GCCTCGGTGGGAGGGAGCATGATCATTTGGTGGTATCGACCACTCGCTATACACGGGCAGT 461

Qy 745 CTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTATCATTTGTGCGGGTGGAG 804
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Db 462 CTCTGGTACACACCCATCCGGCGGGAGTGGTATTATGAAGTGATCATTGTACGTGTGGAA 521

Qy 805 ATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTG 864
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Db 522 ATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAGTACAACCTACGACAAGAGCATTGTG 581

Qy 865 GACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCC 924
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Db 582 GACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAAGTATTTGAAGCTGCCGTCAAGTCC 641

Qy 925 ATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTG 984

Db	642	ATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGATGGCTTTTGGCTAGGGGAGCAGCTG	701
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Db	702	GTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATTTTCCCAGTCATTTCACTTTACCTC	761
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Db	762	ATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACCATCCTTCCTCAGCAATACCTACGG	821
Qy	1105	CCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCA	1164
Db	822	CCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGTTACAAGTTCGCTGTCTCACAGTCA	881
Qy	1165	TCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGG	1224
Db	882	TCCACGGGCACTGTTATGGGAGCCGTCATCATGGAAGGTTTCTATGTCGTCTTCGATCGA	941
Qy	1225	GCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACG	1284
Db	942	GCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACG	1001
Qy	1285	GCAGCGGTGGAAGGCCCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCA	1344
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Qy	1583	CAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCC	1642
Db	1302	TGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCTACCAACCTGCCAATGCTTCTGGC	1361
Qy	1643	TTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAG	1702
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Qy	1703	AAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGT	1762
Db	1421	GAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATATCCTTAGACACCACAACTTGAGT	1480
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Db      1481 -TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACCCTCTGCCCAGCA-TCCTTTAGAGT 1538
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Db      1539 CTCCAACCTAAAGTATTCTTTATGTC---CTTCCAGAAGTACTGGCGTCATACTCAGGCT 1595
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Db      1654 GGCCAAAGTCAGCAGAAGA--AAGTGAAGTTTGCCAGTTGCTTTAGTGATAGGGACTGCA 1711
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RESULT 10

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AF150387
LOCUS      AF150387                      1114 bp      mRNA      linear      EST 22-JUN-1999
DEFINITION AF150387 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone
            CBMAPH03, mRNA sequence.
ACCESSION  AF150387
VERSION    AF150387.1  GI:5133823
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 1114)
  AUTHORS  Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
            Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.
  TITLE    Human mRNA from cd34+ stem cells
  JOURNAL  Unpublished
  COMMENT  Contact: Ye M
            Shanghai Institute of Hematology
            Shanghai Second Medical University, Rui-Jin Hospital
            197 Rui-Jin Road II, Shanghai, 200025, P. R. China
            Email: zchen@stn.sh.cn.
FEATURES   Location/Qualifiers
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BASE COUNT 275 a    300 c    286 g    253 t
ORIGIN

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Query Match          47.9%;  Score 991.6;  DB 9;  Length 1114;
Best Local Similarity 97.4%;  Pred. No. 3.2e-119;
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Qy	772	TGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC	831
Db	61	TGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC	120
Qy	832	TGCAAGGAGTACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG	891
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Qy	892	CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAG	951
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Db	301	TGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC	360
Qy	1072	CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA	1131
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Db	479	ATCATGGAGGGCTTCTACCGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGT	538
Qy	1251	CAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTAC	1310
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Qy	1311	CTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGAC	1370
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Qy	1371	CATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGT	1430
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Db	717	GTGTCAGATGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTATGCTGATGACA	776
Qy	1490	TCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC	1549
Db	777	TCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC	836
Qy	1550	TCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCT	1609

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
 Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
 Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
 Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
 Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
 Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
 Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
 Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
 Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 2504)
 AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
 Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
 Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
 Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
 Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 COMMENT On Dec 10, 2002 this sequence version replaced gi:12852207.
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.

Db	61	CGGCGGGAGTGGTATTATGAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTC	120
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Qy	883	CTTCGTTTGTCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCC	942
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Qy	943	ACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGC	1002
Db	241	ACGGAGAAGTTCCCGGATGGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGC	300
Qy	1003	ACCACCCCTTGGAAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAAC	1062
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Qy	1123	ACGTCCCAAGACGACTGTTTACAAGTTTGGCCATCTCACAGTCATCCACGGGCAGTGTATG	1182
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Qy	1183	GGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGC	1242
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Qy	1303	TTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACC	1362
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Qy	1483	GATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTGGA	1542
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Qy	1543	CCACACCTCCGTGGTTCACTTTGGTCAACA--AGTAGGAGACACAGATGGCACCTGTGGCC	1600
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Qy	1661	GCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGC	1720
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Qy	1901	GTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAG	1960
Db	1194	GTGGTACCCTGGCAGAGAAAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAG	1252
Qy	1961	AGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTG	2020
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RESULT 12

LOCUS BX463709 1025 bp mRNA linear EST 22-MAY-2003

DEFINITION BX463709 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

CS0DN005YN12 3-PRIME, mRNA sequence.

ACCESSION BX463709

VERSION BX463709.1 GI:31033554

KEYWORDS EST.

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1025)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5902.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DN005DG06NP1&cluster=5902.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

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                        vector. Library was not normalized."

BASE COUNT      246 a      249 c      281 g      240 t      9 others
ORIGIN

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Query Match 45.2%; Score 935.8; DB 13; Length 1025;
Best Local Similarity 98.1%; Pred. No. 5.4e-112;
Matches 972; Conservative 5; Mismatches 11; Indels 3; Gaps 3;

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Qy	1245	TGCTGTCTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTT	1304	
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Qy	1305	TGTCACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCT	1364	
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RESULT 13

BQ949536

LOCUS BQ949536 913 bp mRNA linear EST 21-AUG-2002
 DEFINITION AGENCOURT_8733256 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6454803
 5', mRNA sequence.

ACCESSION BQ949536

VERSION BQ949536.1 GI:22365014

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 913)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2632 row: h column: 04
High quality sequence stop: 613.

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 /clone_lib="NIH_MGC_101"
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 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
BASE COUNT 207 a 259 c 232 g 206 t 9 others
ORIGIN

Query Match 39.6%; Score 819.6; DB 13; Length 913;
Best Local Similarity 96.8%; Pred. No. 6e-97;
Matches 864; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

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Qy	1024	CCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATC	1083
Db	121	CCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATC	180
Qy	1084	CTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTAC	1143
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Db	301	TTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCAT	360
Qy	1264	GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATGGAA	1323
Db	361	GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATGGAA	420
Qy	1324	GACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTC	1383

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RESULT 14

BU557282

LOCUS BU557282 928 bp mRNA linear EST 16-SEP-2002

DEFINITION AGENCOURT_10253167 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6585124 5', mRNA sequence.

ACCESSION BU557282

VERSION BU557282.1 GI:22907578

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 928)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

source

Location/Qualifiers

1. .928

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/clone_lib="NIH_MGC_109"
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/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE	COUNT	205	a	254	c	251	g	217	t	1	others
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ORIGIN

Query Match 38.2%; Score 791.2; DB 13; Length 928;

Best Local Similarity 98.1%; Pred. No. 2.8e-93;

Matches 822; Conservative 0; Mismatches 13; Indels 3; Gaps 2;

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Qy	512	TCAACGGCTCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTG	571
Db	94	TCAACGGCTCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTG	153
Qy	572	ACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCT	631
Db	154	ACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCT	213
Qy	632	TCTCCCTGCACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTG	691
Db	214	TCTCCCTGCAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTG	273
Qy	692	TCGGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGT	751
Db	274	TCGGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGT	333
Qy	752	ATACACCCATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATG	811
Db	334	ATACACCCATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATG	393
Qy	812	GACAGGATCTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTG	871
Db	394	GACAGGATCTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTG	453
Qy	872	GCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGG	931

Db 454 GCACCACCAACCTTCGTTTGTCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGG 513
 Qy 932 CAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCT 991
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 Qy 992 GGCAAGCAGGCACCACCCCTTGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTG 1051
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 Db 694 AAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGG 753
 Qy 1172 GCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCC--G 1229
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 Db 754 GCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGA 813
 Qy 1230 AAAACGAATTGGCTTTGCTGTCA-GCGCTTGCCATGTGCACGATGAGTTCAGGACGGC 1286
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 Db 814 AAACGAATTGGGCTTTGCTGTCAAGGCGCTTGCCATGTGCACGATGAAGTCAGGGACGC 871

RESULT 15

AL570757/c

LOCUS AL570757 858 bp mRNA linear EST 31-MAY-2003

DEFINITION AL570757 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI022YF22 3-PRIME, mRNA sequence.

ACCESSION AL570757

VERSION AL570757.2 GI:31292174

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 858)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 16, 2001 this sequence version replaced gi:12927378.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5902.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DI022DC11NP1&cluster=5902.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI022DC11NP1&cluster=5902.r). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI022DC11NP1.

FEATURES Location/Qualifiers

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                 /db_xref="taxon:9606"
                 /clone="CS0DI022YF22"
                 /tissue_type="PLACENTA COT 25-NORMALIZED"
                 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                 /note="1st strand cDNA was primed with a NotI-oligo(dT)
                 primer. Five prime end enriched, double-strand cDNA was
                 digested with Not I and cloned into the Not I and EcoR V
                 sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      214 a      205 c      224 g      200 t      15 others
ORIGIN

Query Match          38.0%; Score 787.4; DB 9; Length 858;
Best Local Similarity 97.2%; Pred. No. 9e-93;
Matches 824; Conservative 5; Mismatches 16; Indels 3; Gaps 3;

Qy      1148 TTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCT 1207
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Db      845 TTSCCATCTCACATTCATCCAC-GGCACTGTTAT-GGAGCTGTTATCAT-GARGGCTTCT 789

Qy      1208 ACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGC 1267
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Db      788 ACWTTGTCTTTGATCGGGCCRGAAAACGAATTGGYTTGCTRTTCAGCGCTTGCCATGTGC 729

Qy      1268 ACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATGGAAGACT 1327
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Db      728 ACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACTTGYACATGGAAGACT 669

Qy      1328 GTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTCATGG 1387
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Db      668 GTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTCATGG 609

Qy      1388 CTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGGCGCTGCC 1447
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Db      608 CTGCCATNTGCGCCCTCTTNATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGGCGCTGCC 549

Qy      1448 TCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAG 1507
          |||||||||||||||||||||||||||||||||||||||
Db      548 TCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAG 489

Qy      1508 GAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGT 1567
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Db      488 GAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGT 429

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Db      428 CACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCA 369

Qy      1628 CCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGT 1687
          |||||||||||||||||||||||||||||||||||||||
Db      368 CCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGT 309

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Qy	1928	GCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTA	1987
Db	68	GCTTGTTTTCCCTGCTNNCCAAATTCAGTAGGAGAGGATGCACANTTTGCTATTTCTTTA	9
Qy	1988	GAGACAGG	1995
Db	8	GAGACAGG	1

Search completed: January 21, 2004, 14:43:37
 Job time : 4456 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 09:28:36 ; Search time 7650 Seconds
(without alignments)
11069.664 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

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- 3: gb_in:*
- 4: gb_om:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query									
No.	Score	Match	Length	DB	ID	Description					
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2	2070	100.0	2070	6	AX378015	AX378015 Sequence					
3	2070	100.0	2070	6	AX573823	AX573823 Sequence					
4	2068.4	99.9	2070	6	AR224093	AR224093 Sequence					
5	2068.4	99.9	2070	6	AR269224	AR269224 Sequence					
6	2068.4	99.9	2070	6	AX700447	AX700447 Sequence					
7	2068.4	99.9	2070	9	AF200343	AF200343 Homo sapi					
8	2062	99.6	2526	6	AX700446	AX700446 Sequence					
9	2062	99.6	2526	9	AF190725	AF190725 Homo sapi					
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12	2032	98.2	2541	6	AR178469	AR178469 Sequence					
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15	2032	98.2	2541	6	E50816	E50816 Aspartate p					
16	2010	97.1	3252	6	AR305033	AR305033 Sequence					
17	2010	97.1	3252	6	AX062111	AX062111 Sequence					
18	2010	97.1	3252	6	AX063201	AX063201 Sequence					
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22	1894.2	91.5	5757	6	AX364933	AX364933 Sequence					
23	1887.2	91.2	1977	6	AR224094	AR224094 Sequence					
24	1887.2	91.2	1977	6	AR269225	AR269225 Sequence					
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31	1788.8	86.4	1979	6	BD127853	BD127853 Primer fo
32	1788.8	86.4	1979	9	AK075049	AK075049 Homo sapi
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35	1644.8	79.5	1747	6	BD139308	BD139308 Extended
36	1554	75.1	4059	10	BC048189	BC048189 Mus muscu
37	1552.4	75.0	2043	6	AR224095	AR224095 Sequence
38	1552.4	75.0	2043	6	AR269226	AR269226 Sequence
39	1552.4	75.0	2043	6	AX105389	AX105389 Sequence
40	1552.4	75.0	2043	6	AX573827	AX573827 Sequence
41	1552.4	75.0	2043	10	AF200346	AF200346 Mus muscu
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ALIGNMENTS

RESULT 1

AX105385

LOCUS AX105385 2070 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 3 from Patent WO0123533.

ACCESSION AX105385

VERSION AX105385.1 GI:13921511

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: WO 0123533-A 3 05-APR-2001;

Pharmacia & Upjohn Company (US)

FEATURES Location/Qualifiers

source 1. .2070
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61
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Qy 121
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 AGCTTT 180

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Db 121
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Qy 181

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Db 241

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Qy 301

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Db 301

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CACA 360

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GGAG 420

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Db 361

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GGAG 420

Qy 421

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CATT 480

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Db 421
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CATT 480

Qy 481
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Db 541
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TATC 720

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Db 661
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TATC 720

Qy 721

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TTAT 780

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Db 721

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Db 781

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Qy 841

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AAA 900

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Db 841

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Qy 901

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Db 901

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Qy 1081

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Db 1081

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|||||

Db 1201

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Qy 1261
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CATG 1320

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Db 1261
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Qy 1321
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TAT 1380

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Db 1321
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TAT 1380

Qy 1381
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Db 1381
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TGG 1440

Qy 1441
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CTG 1500

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Db 1441
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CTG 1500

Qy 1501
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TTCA 1560

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Db 1501

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TTCA 1560

Qy 1561

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CTCC 1620

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Db 1561

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CTCC 1620

Qy 1621

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CCAG 1680

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Db 1621

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CCAG 1680

Qy 1681

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Qy 1801
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GAAG 1920

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Db 1861
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GAAG 1920

Qy 1921
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ATT 1980

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Db 1921
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ATT 1980

Qy 1981
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GA 2040

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Db 1981
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GA 2040

Qy 2041 ATTA 2070

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Db 2041 ATTA 2070

RESULT 2

AX378015

LOCUS AX378015 2070 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 1 from Patent WO0206306.

ACCESSION AX378015

VERSION AX378015.1 GI:19574050

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yan,R., Tomasselli,A.G., Gurney,M.E., Emmons,T.L., Bienkowski,M.J.
and Heinrichson,R.L.

TITLE Substrates and assays for _g(b)-secretase activity

JOURNAL Patent: WO 0206306-A 1 24-JAN-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES Location/Qualifiers

source 1. 2070

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1

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CCCAC 60

Qy 61

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CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

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Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601
CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601
CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

Qy 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841
TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 3

AX573823

LOCUS AX573823 2070 bp DNA linear PAT 07-JAN-2003

DEFINITION Sequence 3 from Patent EP1249498.

ACCESSION AX573823

VERSION AX573823.1 GI:27551477

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses
therefor

JOURNAL Patent: EP 1249498-A 3 16-OCT-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES Location/Qualifiers

source 1. .2070

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

ORIGIN

Query Match 100.0%; Score 2070; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 1801
TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 4

AR224093

LOCUS AR224093 2070 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 3 from patent US 6440698.

ACCESSION AR224093

VERSION AR224093.1 GI:23332753

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
Yan,R.

TITLE Alzheimer's disease secretase, APP substrates therefor, and uses
therefor

JOURNAL Patent: US 6440698-A 3 27-AUG-2002;

FEATURES Location/Qualifiers

source 1. 2070

/organism="unknown"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

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CCCAC 60

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Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCCAACCAAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCCAACCAAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTCCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

|||||

Db 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 5

AR269224

LOCUS AR269224 2070 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 3 from patent US 6500667.

ACCESSION AR269224

VERSION AR269224.1 GI:29700192

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
Yan,R.

TITLE Aspartyl protease 2 (Asp2) antisense oligonucleotides

JOURNAL Patent: US 6500667-A 3 31-DEC-2002;

FEATURES Location/Qualifiers

source 1..2070

/organism="unknown"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CAC 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CAC 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTA 2070

|||||

Db 2041 ATTA 2070

RESULT 6

AX700447

LOCUS AX700447 2070 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 2 from Patent WO03012089.

ACCESSION AX700447

VERSION AX700447.1 GI:29536238

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 2 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. 2070
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801
TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

|||||

Db 1801
TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTA 2070

|||||

Db 2041 ATTA 2070

RESULT 7

AF200343

LOCUS AF200343 2070 bp mRNA linear PRI 12-DEC-1999

DEFINITION Homo sapiens chromosome 11 aspartyl protease 2 mRNA, complete cds.

ACCESSION AF200343

VERSION AF200343.1 GI:6561813

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,
Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
Gurney,M.E.

TITLE Membrane-anchored aspartyl protease with Alzheimer's disease
beta-secretase activity

JOURNAL Nature 402 (6761), 533-537 (1999)

MEDLINE 20057170

PUBMED 10591213

REFERENCE 2 (bases 1 to 2070)

AUTHORS Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301
Henrietta, Kalamazoo, MI 49007, USA

FEATURES Location/Qualifiers

source 1..2070

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="11"

/map="11q23.3-24.1"

CDS 1..1506

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/protein_id="AAF17079.1"

/db_xref="GI:6561814"

/translation="MAQALPWLLWMGAGVLPAGHTQHGIPLRSLGGAPLGLRLP

RETDEEPEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVG

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AAITESDKFFINGSNWEGILGLAYAEIARPDSDLVQTHVPSLQSLCGA

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DCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIAASSTEKFPDGFVLGEQLVCWQAG

TTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGT

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DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRLRQQHDDFADDISLLK"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

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Db 241

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Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

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Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

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GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

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CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

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TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 601
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TTC 660

Qy 661
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TATC 720

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Db 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841
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AAA 900

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Db 841
TACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

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Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

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Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

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Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

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Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

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Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

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Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861

GTAAGTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTAAGTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 8

AX700446

LOCUS AX700446 2526 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 1 from Patent WO03012089.

ACCESSION AX700446

VERSION AX700446.1 GI:29536237

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 1 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. .2526

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 534 a 781 c 715 g 496 t

ORIGIN

Query Match 99.6%; Score 2062; DB 6; Length 2526;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1

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CCCAC 60

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Db 454

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 513

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 514

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 573

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 574

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 633

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 634

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 693

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 694

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 753

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 754

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 813

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 814

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 873

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 874

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 933

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATC
CTG 540

|||||

Db 934

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 993

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 994

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 1053

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 1054

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 1113

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 1114

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 1173

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 1174

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 1233

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 1234

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 1293

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

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Db 1294

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 1353

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 1354

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 1413

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

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Db 1414

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1473

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

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Db 1474
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CC 1533

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CTGT 1140

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Db 1534
ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1593

Qy 1141
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Db 1594
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GAG 1653

Qy 1201
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Db 1654
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TGC 1713

Qy 1261
CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

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Db 1714
CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1773

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

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Db 1774

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1833

Qy 1381

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TGG 1440

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Db 1834

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1893

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

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Db 1894

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1953

Qy 1501

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TTCA 1560

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Db 1954

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2013

Qy 1561

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CTCC 1620

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Db 2014

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CTCC 2073

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

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Db 2074

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 2133

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

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Db 2134

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 2193

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 2194

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 2253

Qy 1801

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

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Db 2254

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
2313

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

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Db 2314
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 2373

Qy 1921
AGACCAAGCTTGTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
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Db 2374
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Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2434
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2493

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2494 ATTAAAAAAAAAACTAGAAAAAAAAAAAAA 2523

RESULT 9

AF190725

LOCUS AF190725 2526 bp mRNA linear PRI 26-OCT-1999

DEFINITION Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete
cds.

ACCESSION AF190725

VERSION AF190725.1 GI:6118538

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2526)

AUTHORS Vassar,R., Bennett,B.D., Babu-Khan,S., Kahn,S., Mendiaz,E.A.,
Denis,P., Teplow,D.B., Ross,S., Amarante,P., Loeloff,R., Luo,Y.,
Fisher,S., Fuller,J., Edenson,S., Lile,J., Jarosinski,M.A.,
Biere,A.L., Curran,E., Burgess,T., Louis,J.C., Collins,F.,
Treanor,J., Rogers,G. and Citron,M.

TITLE Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
the transmembrane aspartic protease BACE

JOURNAL Science 286 (5440), 735-741 (1999)

MEDLINE 20002972

PUBMED 10531052

REFERENCE 2 (bases 1 to 2526)

AUTHORS Bennett,B.D., Vassar,R. and Citron,M.

TITLE Direct Submission

JOURNAL Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center
Dr., Thousand Oaks, CA 91320-1799, USA

FEATURES Location/Qualifiers

source 1. .2526

/organism="Homo sapiens"

/mol_type="mRNA"

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gene 1. .2526

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CDS 454. .1959

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BASE COUNT 534 a 781 c 715 g 496 t

ORIGIN

Query Match 99.6%; Score 2062; DB 9; Length 2526;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2065; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG

CCCAC 60

|||||

Db 454

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG

CCCAC 513

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC

CTGGGG 120

|||||

Db 514

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC

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Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
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Db 574
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
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Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

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Db 634
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 693

Qy 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

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Db 694
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TGCA 753

Qy 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 754
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 813

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 814

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 873

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

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Db 874

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 933

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

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Db 934

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 993

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 994

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 1053

Qy 601

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Db 1054

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TTC 1113

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

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Db 1114

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 1173

Qy 721

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TTAT 780

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Db 1174

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TTAT 1233

Qy 781

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GGAG 840

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Db 1234

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GGAG 1293

Qy 841

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AAA 900

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Db 1294

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AAA 1353

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 1354

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 1413

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

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Db 1414

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CATT 1473

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1474

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CC 1533

Qy 1081

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CTGT 1140

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Db 1534

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1593

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

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Db 1594

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GAG 1653

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

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Db 1654

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TGC 1713

Qy 1261

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CATG 1320

|||||

Db 1714

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CATG 1773

Qy 1321

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TAT 1380

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Db 1774

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1833

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

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Db 1834

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1893

Qy 1441

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CTG 1500

|||||

Db 1894

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1953

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

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Db 1954

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2013

Qy 1561

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CTCC 1620

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Db 2014

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CTCC 2073

Qy 1621

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CCAG 1680

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Db 2074

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CCAG 2133

Qy 1681

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TACT 1740

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Db 2134

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TACT 2193

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 2194

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 2253

Qy 1801

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1860

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Db 2254

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2313

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

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Db 2314

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 2373

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

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Db 2374

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 2433

Qy 1981

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2434

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2493

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2494 ATTAAAAAAAAAACTAGAAAAAAAAAAAAA 2523

RESULT 10

AF201468

LOCUS AF201468 5878 bp mRNA linear PRI 19-DEC-1999

DEFINITION Homo sapiens APP beta-secretase mRNA, complete cds.

ACCESSION AF201468

VERSION AF201468.1 GI:6601444

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5878)

AUTHORS Sinha,S., Anderson,J.P., Barbour,R., Basi,G.S., Caccavello,R.,
Davis,D., Doan,M., Dovey,H.F., Frigon,N., Hong,J.,
Jacobson-Croak,K., Jewett,N., Keim,P., Knops,J., Lieberburg,I.,
Power,M., Tan,H., Tatsuno,G., Tung,J., Schenk,D., Seubert,P.,
Suomensaari,S., Wang,S., Walker,D., Zhao,J., McConlogue,L. and
John,V.

TITLE Purification and cloning of amyloid precursor protein
beta-secretase from human brain

JOURNAL Nature 402 (6761), 537-540 (1999)

MEDLINE 20057171

PUBMED 10591214

REFERENCE 2 (bases 1 to 5878)

AUTHORS Basi,G.S., Power,M.D., Wang,S., Tatsuno,G., Frigon,N., Doan,M.,
Hong,G., Keim,P., Anderson,J., Sinha,S. and McConlogue,L.M.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-1999) Gene Expression Group, Elan

Pharmaceuticals, Inc., 800 Gateway Blvd., S. San Francisco, CA
94080, USA

FEATURES Location/Qualifiers

source 1. .5878

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 /mol_type="mRNA"

 /db_xref="taxon:9606"

 /chromosome="11"

 /map="D11S4352"

 /tissue_type="brain"

CDS 455. .1960

 /function="cleaves APP at the beta-cleavage site"

 /note="membrane type aspartyl protease"

 /codon_start=1

 /product="APP beta-secretase"

 /protein_id="AAF18982.1"

 /db_xref="GI:6601445"

/translation="MAQALPWLLLWMGAGVLPAGHTQHGIPLRSGLGGAFLGLRLP

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BASE COUNT 1547 a 1518 c 1405 g 1408 t

ORIGIN

Query Match 99.2%; Score 2052.6; DB 9; Length 5878;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2055; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1
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Db 455
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CCCAC 514

Qy 61
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CTGGGG 120

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Db 515
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
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Qy 121
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Db 575
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 634

Qy 181
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TGACC 240

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Db 635
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 694

Qy 241

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TGCA 300

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Db 695

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TGCA 754

Qy 301

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CACA 360

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Db 755

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 814

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 815

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GGAG 874

Qy 421

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CATT 480

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Db 875

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 934

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATC
CTG 540

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Db 935

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 994

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 995

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 1054

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 1055

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TTC 1114

Qy 661

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TATC 720

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Db 1115

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 1174

Qy 721

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TTAT 780

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Db 1175

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 1234

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 1235

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 1294

Qy 841

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AAA 900

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Db 1295

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AAA 1354

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 1355

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 1414

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 1415

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CATT 1474

Qy 1021

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CC 1080

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Db 1475

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CC 1534

Qy 1081

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CTGT 1140

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Db 1535

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1594

Qy 1141

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GAG 1200

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Db 1595

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GAG 1654

Qy 1201

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TGC 1260

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Db 1655

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TGC 1714

Qy 1261

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CATG 1320

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Db 1715

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1774

Qy 1321

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TAT 1380

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Db 1775

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1834

Qy 1381

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TGG 1440

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Db 1835

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1894

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

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Db 1895

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1954

Qy 1501

AAGTGAGGAGGCCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

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Db 1955

AAGTGAGGAGGCCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2014

Qy 1561

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CTCC 1620

|||||

Db 2015

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 2074

Qy 1621

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CCAG 1680

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Db 2075

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 2134

Qy 1681

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TACT 1740

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Db 2135

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TACT 2194

Qy 1741

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CT 1800

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Db 2195

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CT 2254

Qy 1801

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1860

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Db 2255

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2314

Qy 1861

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GAAG 1920

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Db 2315

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GAAG 2374

Qy 1921

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ATT 1980

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Db 2375

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ATT 2434

Qy 1981

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2435

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2494

Qy 2041 ATTAAAAAAAAAAAAAAAAA 2059

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Db 2495 ATTAAAAAAAAAACTAGA 2513

RESULT 11

AB032975

LOCUS AB032975 5814 bp mRNA linear PRI 17-MAY-2001

DEFINITION Homo sapiens mRNA for KIAA1149 protein, partial cds.

ACCESSION AB032975

VERSION AB032975.2 GI:14133242

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Hirose, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and
Ohara, O.

TITLE Characterization of cDNA clones selected by the GeneMark analysis
from size-fractionated cDNA libraries from human brain

JOURNAL DNA Res. 6 (5), 329-336 (1999)

MEDLINE 20039618

PUBMED 10574461

REFERENCE 2 (bases 1 to 5814)

AUTHORS Ohara, O., Nagase, T. and Kikuno, R.

TITLE Direct Submission

JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL: <http://www.kazusa.or.jp/huge/>, Tel:438-52-3913,
Fax:438-52-3914)

COMMENT On May 17, 2001 this sequence version replaced gi:6330044.

FEATURES Location/Qualifiers

source 1..5814

/organism="Homo sapiens"

/mol_type="mRNA"

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/note="vector:pBluescriptII SK plus. This sequence is
replaced that of hg01289 cDNA as a representative cDNA
sequence for KIAA1149"

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CQWRCLRLRQQHDDFADDISLLK"

BASE COUNT 1494 a 1510 c 1404 g 1406 t

ORIGIN

Query Match 98.6%; Score 2040; DB 9; Length 5814;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2054; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 1

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Db 443

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CCCAC 502

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCT-
GGGGGGCGCCCCCTGGG 119

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Db 503

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CCTGGG 562

Qy 120

GCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGG
CAGCTT 179

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Db 563

GCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGG
CAGCTT 622

Qy 180

TGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG
ATGAC 239

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Db 623

TGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG
ATGAC 682

Qy 240

CGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACT
TTGC 299

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Db 683

CGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACT
TTGC 742

Qy 300

AGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCA
GCAC 359

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Db 743

AGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCA
GCAC 802

Qy 360

ATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGAAG
GGGA 419

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Db 803

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GGGA 862

Qy 420

GCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCA
ACAT 479

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Db 863

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ACAT 922

Qy 480

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CCT 539

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Db 923

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CCT 982

Qy 540

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ACTC 599

|||||

Db 983

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ACTC 1042

Qy 600

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CTT 659

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Db 1043

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CTT 1102

Qy 660

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GTAT 719

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Db 1103

CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAG
GTAT 1162

Qy 720

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ATTA 779

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Db 1163

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ATTA 1222

Qy 780

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GGA 839

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Db 1223

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GGA 1282

Qy 840

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GAA 899

|||||

Db 1283

GTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAA
GAA 1342

Qy 900

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TGA 959

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Db 1343

AGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCC
TGA 1402

Qy 960

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ACAT 1019

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Db 1403

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ACAT 1462

Qy 1020

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AC 1079

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Db 1463

TTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATC
AC 1522

Qy 1080

CATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACG
ACTG 1139

|||||

Db 1523

CATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACG
ACTG 1582

Qy 1140

TTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GA 1199

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Db 1583

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GA 1642

Qy 1200

GGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGC
TTG 1259

|||||

Db 1643

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TTG 1702

Qy 1260

CCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGG
ACAT 1319

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Db 1703

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ACAT 1762

Qy 1320

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CTA 1379

|||||

Db 1763

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CTA 1822

Qy 1380

TGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA
GTG 1439

|||||

Db 1823

TGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA
GTG 1882

Qy 1440

GCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCT
GCT 1499

|||||

Db 1883

GCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCT
GCT 1942

Qy 1500

GAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTG
GTTC 1559

|||||

Db 1943

GAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTG
GTTC 2002

Qy 1560

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 2003

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 2062

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

|||||

Db 2063

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 2122

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

|||||

Db 2123

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 2182

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 1799

|||||

Db 2183

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 2242

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA
1859

|||||

Db 2243

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA
2302

Qy 1860

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 1919

|||||

Db 2303

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 2362

Qy 1920
GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 2363
GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 2422

Qy 1980
TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

|||||

Db 2423
TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2482

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

|||||

Db 2483 AATTAAAAAAAAAACTAGA 2502

RESULT 12

AR178469

LOCUS AR178469 2541 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 1 from patent US 6319689.

ACCESSION AR178469

VERSION AR178469.1 GI:20219607

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS Powell,D.J., Chapman,C.G., Murphy,K. and Smith,T.S.

TITLE ASP2

JOURNAL Patent: US 6319689-A 1 20-NOV-2001;

FEATURES Location/Qualifiers

source 1..2541

/organism="unknown"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

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Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||||||||||||||||||||||||||||||||||||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTCCCT
GAT 960

|||||||||||||||||||||||||||||||||||||||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||||||||||||||||||||||||||||||||||||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261
CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAAGATAGAGATTCCCCT-
GGACCACACCTCCGTGGTTC 1559

|||||

Db 1501
AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTG
GTTC 1560

Qy 1560

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 1561

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1620

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

|||||

Db 1621

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1680

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

|||||

Db 1681

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1740

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 1799

|||||

Db 1741

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 1800

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA
1859

|||||

Db 1801

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1860

Qy 1860

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 1919

|||||

Db 1861

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAG
AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980

TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

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Db 1981

TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 13

AX002655

LOCUS AX002655 2541 bp DNA linear PAT 10-MAR-2000

DEFINITION Sequence 1 from Patent EP0855444.

ACCESSION AX002655

VERSION AX002655.1 GI:7242133

KEYWORDS .

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS Murphy,K. and Chapman,C.G.

TITLE Aspartic proteinase 2 (ASP2)

JOURNAL Patent: EP 0855444-A 1 29-JUL-1998;

SMITHKLINE BEECHAM PLC (GB); SMITHKLINE BEECHAM CORP (US)

FEATURES Location/Qualifiers

source 1. .2541

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCACGACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601
CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

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Db 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781
GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841
TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841
TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-
GGACCACACCTCCGTGGTTC 1559

|||||

Db 1501

AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTG
GTTC 1560

Qy 1560

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 1561

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1620

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

|||||

Db 1621

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1680

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

|||||

Db 1681

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1740

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAA
CC 1799

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Db 1741

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAA
CC 1800

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1859

|||||

Db 1801

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1860

Qy 1860

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 1919

|||||

Db 1861

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAG
AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980
TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

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Db 1981
TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAAAACTAGA 2060

RESULT 14

AX700452

LOCUS AX700452 2541 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 7 from Patent WO03012089.

ACCESSION AX700452

VERSION AX700452.1 GI:29536241

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 7 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. 2541

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
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Qy 601

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TTC 660

|||||

Db 601

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Qy 661

CCCCCTAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

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Db 661

CCCCCTAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
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Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

||||| ||||||||||||||||||||||||||||||||||||||||

Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

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AAA 900

||||||||||||||||||||||||||||||||||||||||||

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TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
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||||||||||||||||||||||||||||||||||||||||||

Db 901

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GAT 960

Qy 961

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CATT 1020

||||||||||||||||||||||||||||||||||||||||||

Db 961

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CATT 1020

Qy 1021

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CC 1080

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Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

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CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
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Db 1141

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Qy 1201

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Db 1201

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TGC 1260

Qy 1261

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CATG 1320

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Db 1261

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CATG 1320

Qy 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321
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TAT 1380

Qy 1381
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Qy 1620

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|||||

Db 1621

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Qy 1680

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|||||

Db 1681

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Qy 1740

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Db 1741

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Qy 1800

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|||||

Db 1801

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1860

Qy 1860
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GAA 1919

|||||

Db 1861
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AGAA 1920

Qy 1920
GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

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Db 1921
GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980
TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

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Db 1981
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TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 15

E50816

LOCUS E50816 2541 bp DNA linear PAT 18-JUN-2001

DEFINITION Aspartate proteinase ASP2.

ACCESSION E50816

VERSION E50816.1 GI:13023199

KEYWORDS JP 2000060579-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.

TITLE Aspartate proteinase ASP2

JOURNAL Patent: JP 2000060579-A 1 29-FEB-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000060579-A/1

PD 29-FEB-2000

PF 03-AUG-1999 JP 1999219665

PR 28-JAN-1997 GB 9701684:4

PI DAVID J POWERU,CONRAD G CHAPPUMAN,KAY MAFI,TRUDY S SMITH

PC

C12N15/09,A61K31/7088,A61K38/46,A61K39/00,A61K39/395, PC

A61K39/395,A61K48/00,

PC A61P25/28,A61P35/00,A61P43/00,C07K16/40,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12N9/64,C12Q1/37,G01N33/15,G01N33/50,G01N33/53, PC

G01N33/566,

PC G01N33/577//C12P21/08,C12N15/00,A61K37/54,C12N5/00 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .2541

FT /organism='Unidentified'.

FEATURES Location/Qualifiers

source 1. .2541

/organism="unidentified"

/mol_type="genomic DNA"

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BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

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Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
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Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

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Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361
TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421
CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421
CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
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GGACCACACCTCCGTGGTTC 1559

|||||

Db 1501
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Qy 1560
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CCTC 1619

|||||

Db 1561
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Qy 1620

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TCCA 1679

|||||

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TCCA 1680

Qy 1680

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ATAC 1739

|||||

Db 1681

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ATAC 1740

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA

CC 1799

|||||

Db 1741

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA

CC 1800

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA

1859

|||||

Db 1801

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1860

Qy 1860

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GAA 1919

|||||

Db 1861

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAG
AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

|||||

Db 1981

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

|||||

Db 2041 AATTAAAAAAAAAAAACTAGA 2060

Search completed: January 21, 2004, 13:29:20

Job time : 7664 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 09:01:24 ; Search time 579 Seconds
(without alignments)
9650.841 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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			Match	Length					
No.	Score								
1	2070	100.0	2070	21	AAA15662				Human aspartyl pro
2	2070	100.0	2070	22	AAD17865				Human aspartyl pro
3	2070	100.0	2070	22	AAD13021				Human aspartyl pro
4	2070	100.0	2070	22	AAS11517				Human cDNA encodin
5	2070	100.0	2070	22	AAS11702				DNA encoding human
6	2070	100.0	2070	22	AAD06739				Human aspartyl pro
7	2070	100.0	2070	24	ABL52457				Human Asp-2(a) nuc
8	2070	100.0	2070	24	ABL49914				Human aspartyl pro
9	2047.8	98.9	16080	21	AAA59553				DNA clone pCEK C1.
10	2039.8	98.5	2348	21	AAA59551				DNA encoding a hum
11	2032	98.2	2541	19	AAV41696				Nucleotide sequenc
12	2010	97.1	3252	22	AAF31848				Human memapsin 2 c
13	2010	97.1	3252	22	AAF28101				Memapsin 2 DNA. H
14	2010	97.1	3252	24	ABK91244				Human cDNA encodin
15	2010	97.1	3252	24	ABK88641				cDNA encoding huma
16	2010	97.1	3252	25	ABX11591				Human partial cDNA
17	1894.2	91.5	5757	24	ABL39774				Human NS cDNA sequ
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22	1887.2	91.2	1977	22	AAS11703				DNA encoding human
23	1887.2	91.2	1977	22	AAD06740				Human aspartyl pro
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25	1887.2	91.2	1977	24	ABL49915				Human aspartyl pro
26	1843.4	89.1	2370	19	AAV41697				Partial nucleotide
27	1788.8	86.4	1979	22	AAK94824				Human full-length
28	1655.8	80.0	1746	25	ACC51071				Human amyloid proc
29	1644.8	79.5	1747	20	AAX97602				Extended human sec
30	1552.4	75.0	2043	21	AAA15664				Murine aspartyl pr
31	1552.4	75.0	2043	22	AAD17867				Murine aspartyl pr
32	1552.4	75.0	2043	22	AAD13023				Murine aspartyl pr
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34	1552.4	75.0	2043	22	AAS11704				DNA encoding mouse
35	1552.4	75.0	2043	22	AAD06741				Murine aspartyl pr
36	1552.4	75.0	2043	24	ABL52459				Mouse Asp-2(a) nuc
c 37	1501.2	72.5	2907	23	AAS82237				DNA encoding novel
38	1499.8	72.5	1503	21	AAA28278				Human cDNA encodin
39	1499.8	72.5	1503	21	AAA59550				DNA encoding a hum
40	1499.8	72.5	1527	24	ABA02406				FLAG-tagged human
41	1487.4	71.9	1911	22	AAD09485				Human aspartyl pro
42	1423	68.7	2914	23	AAS73798				DNA encoding novel
43	1395.4	67.4	2158	24	ABK63758				Rat sequence diffe
44	1359	65.7	1362	21	AAA15688				Modified human asp
45	1359	65.7	1362	22	AAD17878				Human-Asp 2(a) pro

ALIGNMENTS

RESULT 1

AAA15662

ID AAA15662 standard; cDNA; 2070 BP.

XX

AC AAA15662;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 2 (a) (Asp2) nucleotide sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; ss.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

FF 23-SEP-1999; 99WO-US20881.

XX

PR 24-SEP-1998; 98US-0101594.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR P-PSDB; AAY88425.

XX

PT New enzyme designated human aspartase useful in research into

PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -

XX

PS Claim 5; Fig 2; 183pp; English.

XX

CC This sequence represents the human aspartyl protease 2 (Asp2) nucleotide
CC sequence. The invention relates to a protease (e.g. Asp2) capable of
CC cleaving the beta secretase site of amyloid precursor protein (APP). The
CC protease contains a sequence encoding the amino acid sequence DTG and a
CC sequence encoding DSG or DTG separated by 100-300 amino acids. When
CC mutated the APP gene causes an autosomal dominant form of Alzheimer's
CC disease. APP localises to the cell surface membrane and have a single
CC C-terminal transmembrane domain. Proteolytic processing of APP produces
CC the amyloid beta protein, which is possibly very important in Alzheimer's
CC disease. The invention includes a nucleotide sequence encoding the
CC protease, a vector containing the nucleotide sequence, and a cell line
CC comprising the vector. Methods for screening for inhibitors of beta
CC secretase activity are also given in the invention. The human aspartase
CC protein and nucleotide sequences and the methods for identifying
CC inhibitors of the protease, are useful in the treatment of and research
CC in to Alzheimer's disease.

XX

SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match

100.0%; Score 2070; DB 21; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
        |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db    301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCAGCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480
        |||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540
        |||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        |||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        |||
Db    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC 720
        |||
Db    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
        |||
Db    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
        |||
```

Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680

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Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
          ||||||||||||||||||||||||||||||||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 2

AAD17865

ID AAD17865 standard; cDNA; 2070 BP.

XX

AC AAD17865;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease 2(a) [hu-Asp2(a)] cDNA.

XX

KW Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Human aspartyl protease 2(a)"

FT sig_peptide 1..63

FT /*tag= b

FT mat_peptide 64..1503

FT /*tag= c

FT /product= "Mature human aspartyl protease 2(a)"

XX

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PN      GB2357767-A.
XX
PD      04-JUL-2001.
XX
PF      22-SEP-2000; 2000GB-0023315.
XX
PR      23-SEP-1999;    99US-0155493.
PR      23-SEP-1999;    99US-0404133.
PR      23-SEP-1999;    99WO-US20881.
PR      13-OCT-1999;    99US-0416901.
PR      06-DEC-1999;    99US-0169232.
XX
PA      (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI      Bienkowski MJ,  Gurney M;
XX
DR      WPI; 2001-444208/48.
DR      P-PSDB; AAE10629.
XX
PT      Polypeptide comprising fragments of human aspartyl protease with
PT      amyloid precursor protein processing activity and alpha-secretase
PT      activity, for identifying modulators useful in treating Alzheimer's
PT      disease -
XX
PS      Example 2; Fig 2; 187pp; English.
XX
CC      The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC      Asp1 proteins which lack transmembrane domain or amino terminal
CC      domain or cytoplasmic domain and retains alpha-secretase activity
CC      and amyloid protein precursor (APP) processing activity. The proteins
CC      of the invention are useful for assaying hu-Asp1 alpha-secretase
CC      activity, which in turn is useful for identifying modulators of
CC      hu-Asp1 alpha-secretase activity, where modulators that increase
CC      hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC      disease (AD) which causes progressive dementia with consequent
CC      formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC      neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC      hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC      the substrate under acidic conditions and determining the level of
CC      hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
CC      long form of human Asp2 protein, designated as Asp2(a). Asp2 gene is
CC      localised on chromosome 11q23.3-24.1.
XX
SQ      Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match          100.0%;  Score 2070;  DB 22;  Length 2070;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2070;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCCTGCCCTGCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCCTGCCCTGCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

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Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020

Db	961	 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860

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Db      1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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        |||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
        |||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Qy      2041 ATTA
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Db      2041 ATTA

```

RESULT 3

AAD13021

ID AAD13021 standard; cDNA; 2070 BP.

XX

AC AAD13021;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human aspartyl protease 2a (Hu-Asp2a) cDNA.

XX

KW Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy;
 KW chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

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FT sig_peptide 1..63

FT /*tag= b

FT mat_peptide 64..1503

FT /*tag= c

FT /product= "Mature human aspartyl protease 2a (Hu-Asp2a)"

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00799.

XX

PR 09-MAY-2001; 2001WO-IB00799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

[illegible]

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Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	 GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

Db 1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 4

AAS11517

ID AAS11517 standard; cDNA; 2070 BP.

XX

AC AAS11517;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA encoding Aspartyl protease 2(a), Asp2(a).

XX

KW Human; Aspartyl protease; Asp2(a); beta-secretase; nootropic;

KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KW amyloid-beta; Abeta; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Asp2(a)"

FT sig_peptide 1..63

FT /*tag= b

FT sig_peptide 64..135

FT /*tag= c

FT /label= Pre_pro_peptide

FT sig_peptide 136..171

FT /*tag= d

FT /label= Pro_peptide

FT mat_peptide 172..1503

FT /*tag= e

FT /label= Mature_Asp2(a)

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00798.

XX

PR 09-MAY-2001; 2001WO-IB00798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCC'TGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCC'TGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCAC'TGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCAC'TGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCA'ACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCA'ACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGT'CGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGT'CGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTG'AAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTG'AAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
 |||
 Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
 |||
 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
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 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320

Qy 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
 |||
 Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG 1440
 |||
 Db 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG 1440

Qy 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
 |||
 Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGTGGTTCA 1560
 |||
 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 |||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
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 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
 |||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 |||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 |||
 Db 1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 |||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

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      |||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
      |||
Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
      |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
      |||
Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
      |||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 5

AAS11702

ID AAS11702 standard; DNA; 2070 BP.

XX

AC AAS11702;

XX

DT 24-OCT-2001 (first entry)

XX

DE DNA encoding human aspartyl protease 2a (Asp-2a).

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Aspartyl protease-2a (Asp-2a)"

FT sig_peptide 1..63

FT /*tag= b

FT misc_feature 64..135

FT /*tag= c

FT /note= "Pre-propeptide"

FT misc_feature 136..171

FT /*tag= d

FT /note= "Propeptide"

FT mat_peptide 172..1503

FT /*tag= e

FT /note= "Mature Aspartyl protease-2a"

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00797.

XX

PR 09-MAY-2001; 2001WO-IB00797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.


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XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR P-PSDB; AAU07102.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 98; Fig 2; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the
CC coding sequence of human Asp-2a used in the methods of the invention.
XX
SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match          100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      |
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      |
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGGCAGCTTT 180
      |
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      |
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

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Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321		GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321		GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGGACCACACCTCCGTGGTTCA	1560
Db	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGGACCACACCTCCGTGGTTCA	1560
Qy	1561		CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561		CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621		CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621		CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681		GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681		GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741		CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741		CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801		TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801		TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861		GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861		GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921		AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 6

AAD06739

ID AAD06739 standard; cDNA; 2070 BP.

XX

AC AAD06739;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human aspartyl protease 2a (Asp2a) cDNA.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp 2a;

KW beta-secretase; chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Human aspartyl protease 2a"

FT sig_peptide 1..63

FT /*tag= b

FT sig_peptide 64..135

FT /*tag= c

FT /note= "Pre-pro-peptide"

FT sig_peptide 136..171

FT /*tag= d

FT /note= "Pro-peptide"

FT mat_peptide 172..1503

FT /*tag= e

FT /product= "Human mature aspartyl protease 2a"

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US26080.

XX

PR 23-SEP-1999; 99US-0155493.

PR 23-SEP-1999; 99WO-US20881.

PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

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XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02581.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 2; Page 126-127; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease
CC   (Asp) 2a cDNA. Asp 2a has beta-secretase protease activity. Asp2 gene
CC   is located on chromosome 11q23.3-24.1.
XX
SQ   Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match          100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy      241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        |||
Db      241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy      301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db      301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy      361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db      361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy      421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
        |||
Db      421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy      481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

```

Db	481	 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380

Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA GTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA GTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 7

ABL52457

ID ABL52457 standard; cDNA; 2070 BP.

XX

AC ABL52457;

XX

DT 16-JUL-2002 (first entry)
 XX
 DE Human Asp-2(a) nucleotide sequence SEQ ID NO:3.
 XX
 KW Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
 KW proteolytic; chromosome 11q23.3-24.1; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1506
 FT /*tag= a
 FT /product= "Asp-2(a)"
 FT /note= "aspartyl protease"
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-0025934.
 XX
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2002-396337/43.
 DR P-PSDB; ABB78590.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease -
 XX
 PS Example 2; Fig 2; 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or

CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence encodes hu-Asp2(a) from the present invention.

XX

SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 24; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
```

Qy	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 8

ABL49914

ID ABL49914 standard; DNA; 2070 BP.

XX

AC ABL49914;

XX

DT 31-MAY-2002 (first entry)

XX

DE Human aspartyl protease nucleotide sequence SEQ ID NO:1.

XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;

KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;

KW Alzheimer's disease; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200206306-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23035.
 XX
 PR 19-JUL-2000; 2000US-219795P.
 PR 12-MAR-2001; 2001US-275251P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;
 XX
 DR WPI; 2002-216995/27.
 DR P-PSDB; ABB06409.
 XX
 PT Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 XX
 PS Claim 1; Page 117; 188pp; English.
 XX
 CC The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

 Query Match 100.0%; Score 2070; DB 24; Length 2070;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

 Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

 Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGCCGGAGGGGCAGCTTT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGCCGGAGGGGCAGCTTT 180

 Qy 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Db	181		GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Db	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Qy	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAAATGGACTGCAAGGAG	840
Db	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAAATGGACTGCAAGGAG	840
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 |||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 |||
 Db 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 9

AAA59553

ID AAA59553 standard; DNA; 16080 BP.

XX

AC AAA59553;

XX

DT 14-NOV-2000 (first entry)

XX

DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor; ss.

XX

OS Homo sapiens.

XX

PN WO200047618-A2.

XX

PD 17-AUG-2000.

XX

PF 10-FEB-2000; 2000WO-US03819.

XX

PR 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX

DR WPI; 2000-533011/48.

XX

PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease -

XX

PS Disclosure; Fig 13A-E; 121pp; English.

XX

CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to

CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.

XX

SQ Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;

Query Match 98.9%; Score 2047.8; DB 21; Length 16080;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1675 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 1734

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1735 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 1794

Qy     121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1795 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 1854

Qy     181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1855 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 1914

Qy     241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1915 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 1974

Qy     301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1975 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 2034

Qy     361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2035 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 2094

Qy     421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2095 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 2154

Qy     481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2155 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 2214

Qy     541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2215 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 2274

Qy     601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2275 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 2334

Qy     661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Db	2335		CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	2394
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	2395		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	2454
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	2455		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	2514
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	2515		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	2574
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	2575		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	2634
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	2635		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	2694
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	2695		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	2754
Qy	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	2755		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	2814
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	2815		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	2874
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	2875		GCCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	2934
Qy	1261		CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	2935		CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	2994
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Db	2995		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	3054
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	3055		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	3114
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	3115		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	3174
Qy	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCCTGGACCACACCTCCGTGGTTCA	1560

Db	3175	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTC	3234
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	3235	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	3294
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	3295	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	3354
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	3355	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	3414
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	3415	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	3474
Qy	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	3475	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	3534
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	3535	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	3594
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	3595	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	3654
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	3655	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	3714
Qy	2041	ATTAAAAAAAAAAAAAAAAA	2059
Db	3715	ATTAAAAAAAAAAAACTAGA	3733

RESULT 10

AAA59551

ID AAA59551 standard; DNA; 2348 BP.

XX

AC AAA59551;

XX

DT 14-NOV-2000 (first entry)

XX

DE DNA encoding a human beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 306..1811

Db	486	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	545
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	546	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	605
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	606	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	665
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	666	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	726	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	785
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	845
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	846	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	905
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	906	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	965
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	966	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	1025
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	1085
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	1086	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1145
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	1146	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	1205
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	1206	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	1265
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1325
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1326	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1385

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1386	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1445
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1446	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1505
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1506	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1565
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1566	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1625
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1626	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1685
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA GTGG	1440
Db	1686	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA GTGG	1745
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1746	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1805
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1806	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1865
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCTCC	1620
Db	1866	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCTCC	1925
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1926	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1985
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1986	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	2045
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	2046	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	2105
Qy	1801	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	2106	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	2165
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	2166	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	2225

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 2226 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 2285

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 |||
 Db 2286 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2345

Qy 2041 ATT 2043
 |||
 Db 2346 ATT 2348

RESULT 11

AAV41696

ID AAV41696 standard; cDNA; 2541 BP.

XX

AC AAV41696;

XX

DT 26-OCT-1998 (first entry)

XX

DE Nucleotide sequence of human ASP2 (aspartic protease 2).

XX

KW Human; ASP2; aspartic protease 2; agonist; antagonist; immunospecific;
 KW antibody; inhibition; Alzheimer's disease; cancer; proteinase;
 KW prohormone processing; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1..1506
FT		/*tag= a
FT		/product= "human ASP2"

XX

PN EP855444-A2.

XX

PD 29-JUL-1998.

XX

PF 27-JAN-1998; 98EP-0300573.

XX

PR 28-JAN-1997; 97GB-0001684.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Chapman CG, Murphy K, Powell DJ, Smith TS;

XX

DR WPI; 1998-389809/34.

DR P-PSDB; AAW59807.

XX

PT New nucleic acid encoding human aspartic protease 2 - used to treat,
 PT prevent and diagnose e.g. Alzheimer's disease, cancer and prohormone
 PT processing

XX

PS Claim 2; Pages 6-7; 26pp; English.

XX

CC This is the nucleotide sequence of the human ASP2 (aspartic protease 2),

CC used in the method of the invention. Agonists and antagonists for
CC ASP2 immunospecific antibodies are used to treat conditions requiring
CC increased or decreased activity or expression of ASP2 respectively.
CC ASP2 is used to treat and diagnose e.g. Alzheimer's disease, cancer
CC and prohormone processing and ASP2 or a fragment can be used to induce
CC an immune response against the above conditions.

XX

SQ Sequence 2541 BP; 598 A; 673 C; 675 G; 579 T; 16 other;

Query Match 98.2%; Score 2032; DB 19; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

```
Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
```

Qy	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC	1559

PD 04-JAN-2001.
 XX
 PF 27-JUN-2000; 2000WO-US17742.
 XX
 PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178368.
 PR 08-JUN-2000; 2000US-0210292.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Tang JJN, Hong L, Ghosh AK;
 XX
 DR WPI; 2001-137933/14.
 DR P-PSDB; AAB66572.
 XX
 PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
 PT having 2 catalytic aspartic residues and substrate binding cleft, used
 PT to treat Alzheimer's disease by blocking amyloid precursor protein
 PT cleavage -
 XX
 PS Example 1; Page 70-71; 86pp; English.
 XX
 CC The present sequence is given in a specification relating to an inhibitor
 CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
 CC active site, which is defined by the presence of two catalytic aspartic
 CC residues and a substrate binding cleft. The inhibitor is useful for
 CC the treatment and diagnosis of Alzheimer's disease. It is useful in
 CC screens for individuals with a genetic predisposition to Alzheimer's
 CC disease. The inhibitor is useful as a reagent for specifically binding to
 CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
 CC isolation, purification and characterisation.
 XX
 SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 22; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	40	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	99
Db	1	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	60
Qy	100	CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG	159
Db	61	CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG	120
Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240

Qy 280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 339
 |||
 Db 241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 300

Qy 340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
 |||
 Db 301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy 400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 459
 |||
 Db 361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 420

Qy 460 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
 |||
 Db 421 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy 520 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
 |||
 Db 481 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy 580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
 |||
 Db 541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy 640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG 699
 ||
 Db 601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG 660

Qy 700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
 |||
 Db 661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy 760 ATCCGGCGGGAGTGGTATTATGAGGTATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
 |||
 Db 721 ATCCGGCGGGAGTGGTATTATGAGGTATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy 820 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC 879
 |||
 Db 781 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy 880 AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
 |||
 Db 841 AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy 940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
 |||
 Db 901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy 1000 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
 |||
 Db 961 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy 1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
 |||
 Db 1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy 1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179

Db	1081	 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTCAAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	 TGCCTCATGGTGTGTCAAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACCTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	 GGACCACACCTCCGTGGTTCACCTTGGTCAACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	 GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1899
Db	1801	 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861	 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1920
Qy	1960	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	2019

Db 1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy 2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAAAAA 2057
 ||| |

Db 1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAACACTAGA 2018

RESULT 13

AAF28101

ID AAF28101 standard; DNA; 3252 BP.

XX

AC AAF28101;

XX

DT 02-APR-2001 (first entry)

XX

DE Memapsin 2 DNA.

XX

KW Memapsin 2; catalyst; Alzheimer's; ds.

XX

OS Homo sapiens.

XX

PN WO200100663-A2.

XX

PD 04-JAN-2001.

XX

PF 27-JUN-2000; 2000WO-US17661.

XX

PR 28-JUN-1999; 99US-0141363.

PR 30-NOV-1999; 99US-0168060.

PR 25-JAN-2000; 2000US-0177836.

PR 27-JAN-2000; 2000US-0178368.

PR 08-JUN-2000; 2000US-0210292.

XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX

PI Tang JJN, Lin X, Koelsch G;

XX

DR WPI; 2001-102885/11.

XX

PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease -

XX

PS Example 1; Page 71-72; 86pp; English.

XX

CC The present invention relates to a purified recombinant
 CC catalytically active memapsin 2. The invention may be used for
 CC isolating inhibitors which are used to treat or prevent
 CC Alzheimer's disease. The invention may also be used to screen
 CC for individuals more genetically prone to develop Alzheimer's
 CC disease.

XX

SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 22; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	40	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	99
Db	1	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	60
Qy	100	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	159
Db	61	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	120
Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCA ACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCA ACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840

Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779

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Db      1681  |||||CTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740
Qy      1780  TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT 1839
Db      1741  |||||TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT 1800
Qy      1840  CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
Db      1801  |||||CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860
Qy      1900  TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
Db      1861  |||||TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy      1960  GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db      1921  |||||GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020  GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
Db      1981  |||||GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 14

ABK91244

ID ABK91244 standard; cDNA; 3252 BP.

XX

AC ABK91244;

XX

DT 15-NOV-2002 (first entry)

XX

DE Human cDNA encoding Memapsin 2.

XX

KW Human; ss; gene; memapsin 2; aspartic protease; beta secretase;
KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
KW APP; neuroprotective; nootropic; inhibitor;
KW substrate side-chain preference.

XX

OS Homo sapiens.

XX

PN WO200253594-A2.

XX

PD 11-JUL-2002.

XX

PF 28-DEC-2001; 2001WO-US50826.

XX

PR 28-DEC-2000; 2000US-258705P.

PR 14-MAR-2001; 2001US-275756P.

XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNII) UNIV ILLINOIS FOUND.

XX

PI Tang JJN, Koelsch G, Ghosh AK;

XX

DR WPI; 2002-619088/66.

DR P-PSDB; ABG78372, ABG78374.

XX
PT New memapsin 2 activity inhibitor useful in treatment of e.g.
PT Alzheimer's disease -
XX
PS Disclosure; Fig 6; 74pp; English.
XX
CC The invention relates to an inhibitor of catalytically active memapsin 2
CC (an aspartic protease which can cleave at beta secretase sites), which
CC binds to the active site of memapsin 2 defined by the presence of two
CC catalytic aspartic residues and substrate binding cleft. Also
CC included is a method of determination of the substrate side-chain
CC preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of
CC memapsin 2 substrates with memapsin 2, and determining the sub-site
CC preference of memapsin 2 by determining relative initial hydrolysis rates
CC of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial
CC library of memapsin 2 inhibitors containing a base sequence taken from
CC OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of
CC inhibitors with memapsin 2 which binds to several inhibitors to generate
CC several bound memapsin 2, and detecting the bound memapsin 2 with an
CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
CC secondary antibody. The inhibitors may be used in the manufacture of a
CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
CC be involved in the cleavage of amyloid precursor protein (APP), and for
CC determining the substrate side-chain preference in memapsin 2 sub-sites.
CC The present sequence encodes human memapsin 2.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy	100	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	159
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Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
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Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459

Db	361		CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
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Qy	520		TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481		TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580		CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
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Qy	640		CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	699
Db	601		CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	660
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Qy	760		ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721		ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000		GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
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Qy	1060		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
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Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
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Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
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Qy	1660	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1959
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Qy	1960	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	2019
Db	1921	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	1980
Qy	2020	GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA	2057
Db	1981	GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA	2018

ID ABK88641 standard; cDNA; 3252 BP.
XX
AC ABK88641;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA encoding human memapsin 2.
XX
KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1467
FT /*tag= a
FT /partial
FT /product= "Memapsin 2"
FT /note= "This sequence lacks a start codon"
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PN US2002049303-A1.
XX
PD 25-APR-2002.
XX
PF 28-FEB-2001; 2001US-0796264.
XX
PR 28-JUN-1999; 99US-141363P.
PR 30-NOV-1999; 99US-168060P.
PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX
PA (TANG/) TANG J J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX
PI Tang JJN, Lin X, Koelsch G, Hong L;
XX
DR WPI; 2002-507280/54.
DR P-PSDB; AAU99488.
XX
PT New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease -
XX
PS Example 1; Page 20-21; 44pp; English.
XX
CC The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence encodes

CC human memapsin 2.

XX

SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy      40 GCGGGAGTGCTGCCTGCCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
          |||
Db       1 GCGGGAGTGCTGCCTGCCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy     100 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
          |||
Db      61 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120

Qy     160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
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Db     121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy     220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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Db     181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy     280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC 339
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Db     241 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC 300

Qy     340 CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
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Db     301 CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy     400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
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Db     361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 420

Qy     460 GTCACGTGTCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
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Db     421 GTCACGTGTCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy     520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
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Db     481 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy     580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
          |||
Db     541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy     640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG 699
          ||
Db     601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG 660

Qy     700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
          |||
Db     661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy     760 ATCCGGCGGGAGTGGTATTATGAGGTCATCATTTGTGCGGGTGGAGATCAATGGACAGGAT 819
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Db	721		ATCCGGCGGGAGTGGTATTATGAGGTGATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000		GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961		GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1119
Db	1021		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1080
Qy	1120		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240		GGCTTTGCTGTGCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
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Db	1261		CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360		ACCCTCATGACCATAGCCTATGTGATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
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Qy	1420		TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381		TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480		GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441		GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540		GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
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GenCore version 5.1.6
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4	2032	98.2	2541	4	US-09-009-191-1		Sequence 1, Appli
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6	1887.2	91.2	1977	4	US-09-548-372D-5		Sequence 5, Appli
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16	1359	65.7	1380	4	US-09-548-372D-31	Sequence 31, Appl
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26	1273.6	61.5	1302	4	US-09-548-372D-25	Sequence 25, Appl
27	1273.6	61.5	1302	4	US-09-548-367D-25	Sequence 25, Appl
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35	1183.2	57.2	1278	4	US-09-548-372D-27	Sequence 27, Appl
36	1183.2	57.2	1278	4	US-09-548-367D-27	Sequence 27, Appl
37	1183.2	57.2	1278	4	US-09-551-853D-27	Sequence 27, Appl
38	421.2	20.3	511	4	US-09-280-116-30	Sequence 30, Appl
39	393.4	19.0	1545	3	US-09-717-432-1	Sequence 1, Appli
40	393.4	19.0	1545	4	US-09-912-484-1	Sequence 1, Appli
41	393.4	19.0	1804	4	US-09-548-372D-1	Sequence 1, Appli
42	393.4	19.0	1804	4	US-09-548-367D-1	Sequence 1, Appli
43	393.4	19.0	1804	4	US-09-551-853D-1	Sequence 1, Appli
44	391.8	18.9	1862	3	US-08-999-723-1	Sequence 1, Appli
45	391.8	18.9	1862	3	US-09-434-427-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-548-372D-3

; Sequence 3, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/62801

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
        |||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT 480
        |||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
        |||||||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        |||||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        |||||||
Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
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Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 |||
 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 |||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 |||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
 |||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 |||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 |||
 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 |||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 |||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 2

US-09-548-367D-3

; Sequence 3, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC	60
Qy	61	GGCACCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660

Db	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261		CATGTGCACGATGAGTTTCTAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261		CATGTGCACGATGAGTTTCTAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
 Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
 Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 Qy 1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
 Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 Qy 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 ||||||||||||||||||||||||||||||||
 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 3

US-09-551-853D-3

; Sequence 3, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-3
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Query Match          99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
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Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACGTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACGTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440

Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 4

US-09-009-191-1

; Sequence 1, Application US/09009191

; Patent No. 6319689

; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID

; APPLICANT: CHAPMAN, CONRAD

; APPLICANT: MURPHY, KAY

; APPLICANT: SMITH, TRUDI

; TITLE OF INVENTION: ASP2

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

```

; ADDRESS: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-1

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Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC	1559
Db	1501	AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1619
Db	1561	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATCTGCTGCTTGAAACTTCAGCCCTGAACC	1799
Db	1741	TCTTGGTCACCTCAAATTTAAGTCGGGAAATCTGCTGCTTGAAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1859
Db	1801	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCTTGGCAGAGAA	1919
Db	1861	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979
Db	1921	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1980

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Qy      1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
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Db      1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy      2040 AATTAAAAAAAAAAAAAAAAAAAA 2059
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Db      2041 AATTAAAAAAAAAAAACTAGA 2060

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RESULT 5

US-09-604-608-1

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; Sequence 1, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-608-1

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Query Match          97.1%; Score 2010; DB 4; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGC 99
          |||
Db      1  GCGGGAGTGCTGCCTGCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGC 60

Qy     100 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
          |||
Db      61 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy     160 CCCGCGCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAG 219
          |||
Db     121 CCCGCGCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAG 180

Qy     220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

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Db	181	 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAAC'TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	 ACAGGCAGCAGTAAC'TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	 CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	699
Db	601	 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	660
Qy	700	AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	 AGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	 AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	 GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119

Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGACGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGACGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1920


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Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
          |||
Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
          |||
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 6

US-09-548-372D-5

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; Sequence 5, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-5

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Query Match          91.2%; Score 1887.2; DB 4; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
          |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180
          |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
          |||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

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Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1785
Qy	1861	GTA CTGGCATCACACG CAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1786	GTA CTGGCATCACACG CAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1845
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

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Db      1846  |||||
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy      1981  TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
|||||

Db      1906  TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965
|||||

Qy      2041  ATTAAAAAAAAA 2052
| |||||

Db      1966  AAAAAAAAAA 1977

```

RESULT 7

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US-09-548-367D-5
; Sequence 5, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-5

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Query Match          91.2%; Score 1887.2; DB 4; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy      1  ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
|||||

Db      1  ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
|||||

Qy      61  GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
|||||

Db      61  GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
|||||

Qy      121  CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
|||||

Db      121  CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
|||||

Qy      181  GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

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Db	181		GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Db	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Qy	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541		GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568		-----CTTTGTGGTGCTGGCTTC	585
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781		GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706		GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTGAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTGAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCAC'TCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCAC'TCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1785
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1786	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1845

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Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
        |||
Db      1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
        |||
Db      1906 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy      2041 ATTAAAAAAAAA 2052
        | |||
Db      1966 AAAAAAAAAA 1977

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RESULT 8

US-09-551-853D-5

; Sequence 5, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1977

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-551-853D-5

Query Match 91.2%; Score 1887.2; DB 4; Length 1977;

Best Local Similarity 96.2%; Pred. No. 0;

Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

```

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
        |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180

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Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945

Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1785
Qy	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

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Db      1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy      1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1846 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1906 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy      2041 ATTAATAAAAAAAAA 2052
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Db      1966 AAAAAAAAAAAAAA 1977

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RESULT 9

US-09-009-191-3

; Sequence 3, Application US/09009191

; Patent No. 6319689

; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID

; APPLICANT: CHAPMAN, CONRAD

; APPLICANT: MURPHY, KAY

; APPLICANT: SMITH, TRUDI

; TITLE OF INVENTION: ASP2

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,191

; FILING DATE: 20-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 9701684.4

; FILING DATE: 28-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2370 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-3

Query Match 89.1%; Score 1843.4; DB 4; Length 2370;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1867; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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Qy      172 GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 231
          |||
Db       1  GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 60

Qy      232 GAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 291
          |||
Db       61 GAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 120

Qy      292 AACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 351
          |||
Db      121 AACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 180

Qy      352 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGG 411
          |||
Db      181 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGG 240

Qy      412 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGT 471
          |||
Db      241 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGT 300

Qy      472 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 531
          |||
Db      301 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 360

Qy      532 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCGTGACGACTCCCTGGAGCCTTTC 591
          |||
Db      361 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCGTGACGACTCCCTGGAGCCTTTC 420

Qy      592 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGT 651
          |||
Db      421 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGT 480

Qy      652 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATT 711
          |||
Db      481 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATT 540

Qy      712 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 771
          |||
Db      541 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 600

Qy      772 TGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 831
          |||
Db      601 TGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 660

Qy      832 TGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 891
          |||
Db      661 TGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 720
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Qy	892	CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGAGAAG	951
Db	721	CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGGAGAAG	780
Qy	952	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	1011
Db	781	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	840
Qy	1012	TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC	1071
Db	841	TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC	900
Qy	1072	CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA	1131
Db	901	CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA	960
Qy	1132	GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT	1191
Db	961	GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT	1020
Qy	1192	ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC	1251
Db	1021	ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC	1080
Qy	1252	AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACC	1311
Db	1081	AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACC	1140
Qy	1312	TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC	1371
Db	1141	TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC	1200
Qy	1372	ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG	1431
Db	1201	ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG	1260
Qy	1432	TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATC	1491
Db	1261	TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGACAATGGATGACTTTGCTGATGACATC	1320
Qy	1492	TCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCT	1550
Db	1321	TCCCTGCTGAAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCT	1380
Qy	1551	CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC	1610
Db	1381	CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC	1440
Qy	1611	AGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG	1670
Db	1441	AGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG	1500
Qy	1671	TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGG	1730
Db	1501	TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGG	1560

Qy 1731 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1790
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 Db 1561 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1620
 Qy 1791 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1850
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 Db 1621 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1680
 Qy 1851 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCT 1910
 |||
 Db 1681 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCG 1740
 Qy 1911 GGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1970
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 Db 1741 GGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1800
 Qy 1971 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 2030
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 Db 1801 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 1860
 Qy 2031 TGCCTCTTGAATTAAAAAAAAAAAAAAAAA 2059
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 Db 1861 TGCCTCTTGAATTAAAAAAAAAACTAGA 1889

RESULT 10

US-09-548-372D-7

; Sequence 7, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-548-372D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC	60
Db	1	ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCCAG	60
Qy	61	GGCACCCAGCACGGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGAACCCATCTCGGCATCCGGCTGCCCCCTTCGCAGCGGCCCTGGCAGGGCCACCCCTGGGC	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGGGCTGCCCCACACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACCTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGGCATCCTA	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCCGACGACTCTTTGGAGCCCTTCTTTGACTCC	600
Qy	601	CTGGTAAAGCAGACCACGTTCCCAACCTCTTCTCCCTGCACCTTGTGGTGCTGGCTTC	660
Db	601	CTGGTGAAGCAGACCACATTCCTTCCCTGCAGCTCTGTGGCGCTGGCTTC	660
Qy	661	CCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAAGTGATCATTGTACGTGTGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGGCCAAGAAA	900

Db	841		TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901		GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT	960
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961		GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1020
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021		TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081		ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141		TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA	1200
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201		GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAAGCAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261		CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGAAGGTCCGTTTGTTACGGCAGACATG	1320
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321		GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381		GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTGTCAGTGG	1440
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441		CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501		AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC	1560
Qy	1561		CTTTGGTCAACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561		CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619		CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678
Db	1621		CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	1679
Qy	1679		AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA	1738

Db 1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739

Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
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Db 1740 TCCTTAGGCACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798

Qy 1799 CTTTGTCCACCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
 || || ||| || ||||| | ||||| ||||| ||||| | || || |||

Db 1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854

Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || ||| ||| ||| ||||| ||||| ||||| ||||| |||

Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913

Qy 1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
 | | ||| | | ||||| ||||| || ||| | || ||||| |

Db 1914 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970

Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029

Qy 2039 GAATTAAAAA 2052
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Db 2030 GAGATAACAAGAA 2043

RESULT 11

US-09-548-367D-7

; Sequence 7, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-548-367D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
 Best Local Similarity 87.6%; Pred. No. 0;

Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60
        ||||| ||| ||| ||||| ||||| ||| ||||| |||||
Db      1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGAATGCTGCCTGCCAG 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        || ||||| | ||||| ||||| ||||| ||||| ||| | |||||
Db     61 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||| ||||| ||||| ||||| || | ||||| ||||| |||||
Db    121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCGGGCCAGGGCTACTATGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        || ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
Db    241 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 GTGGGGGCTGCCCCACACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGAA 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db    421 CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
        ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
Db    481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAAGTGGGAGGGCATCCTA 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCCGACGACTCTTTGGAGCCTTCTTTGACTCC 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    601 CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
        ||||| ||||| ||| ||| ||||| || ||||| ||||| |||||
Db    661 CCCCTCAACCAGACCGAGGCAGTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 GACCACTCGCTATACACGGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db    781 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840
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Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCCCTTGGAACATT	1020
Db	961	GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTCGTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTATCATGGAA	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201	GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAAGCGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCGGCAGTGAAGGTCCGTTTGTTACGGCAGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCCTGGACCACATCTGGGTGGTTCC	1560
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678
Db	1621	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	1679

Qy 1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
 |||| || ||||| |||| | || |||| ||| ||| |||| |||| |||||
 Db 1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739
 Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC 1798
 ||| | |||| |||| || || ||| ||||| ||||| ||||| ||||| ||||| |
 Db 1740 TCCTTAGGCACCACAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798
 Qy 1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
 || || ||| || ||||| | ||||| ||||| ||||| || || || |||
 Db 1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854
 Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || ||| |||| ||| ||||| ||||| ||||| ||||| |||||
 Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913
 Qy 1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
 | | |||| | | ||||| ||||| || ||| | || ||||| |
 Db 1914 AAGGGCCAATC-TCATTCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970
 Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
 ||||| || ||||| | | ||||| ||| |||| ||||| ||| ||||
 Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029
 Qy 2039 GAATTAATAAAAAAAAA 2052
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 Db 2030 GAGATAAACAAGAA 2043

RESULT 12

US-09-551-853D-7

; Sequence 7, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-551-853D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60
      ||||| ||| ||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Db      1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCAG 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      || ||||| | ||||| ||||| ||||| ||||| ||| | |||||
Db     61 GGAACCCATCTCGGCATCCGGCTGCCCTTTCGACGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      ||| ||||| ||||| ||||| ||| | ||||| ||||| |||||
Db    121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||| ||||| ||||| ||||| ||| || ||||| ||||| |||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
      || ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
Db    241 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 GTGGGGGCTGCCCCACACCTTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGA 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAACATT 480
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Db    421 CTGGGCACCGACCTGGTGAAGCATCCCTCATGGCCCCAACGTCCTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAAGTGGGAGGGGCATCCTA 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCGACGACTCTTGGAGCCCTTCTTTGACTCC 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    601 CTGGTGAAGCAGACCCACATTCCTCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy    661 CCCCTCAACAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    661 CCCCTCAACAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 GACCACTCGCTATACAGGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db	781	GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAACATT	1020
Db	961	GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTCGTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGTTTCTATGTCGTCTTCGATCGAGCCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCGGCAGTGAAGGTCCGTTTGTTACGGCAGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTAGTGG	1440
Db	1381	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC	1560
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678

Db 1621 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC 1679
 Qy 1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
 ||| | | ||||| ||| | | ||| ||| ||| ||| ||| ||| |||
 Db 1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739
 Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
 ||| | ||| ||| || | ||| ||||| ||||| ||||| ||||| |||
 Db 1740 TCCTTAGGCACCACAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798
 Qy 1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
 || || ||| || ||||| | ||||| ||||| ||||| || || |||
 Db 1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854
 Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || ||| ||| ||| ||||| ||||| ||||| |||||
 Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913
 Qy 1919 AGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
 | | ||| | | ||||| ||||| ||||| || ||| | || ||||| |
 Db 1914 AAGGGCCAATC-TCATTCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970
 Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
 ||||| || ||||| | | ||||| ||| ||| ||||| ||| |||
 Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029
 Qy 2039 GAATTAATAAAAAA 2052
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 Db 2030 GAGATAAACAAGAA 2043

RESULT 13

US-09-548-372D-29

; Sequence 29, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 29

; LENGTH: 1362

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 65.7%; Score 1359; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
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Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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 Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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 Db 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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 Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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 Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
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 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320

Qy 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
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 Db 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359

RESULT 14

US-09-548-367D-29

; Sequence 29, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133


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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-29
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Query Match          65.7%; Score 1359; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

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Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
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Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
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US-09-551-853D-29

; Sequence 29, Application US/09551853D

; Patent No. 6500667

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; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-29

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Query Match          65.7%; Score 1359; DB 4; Length 1362;
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2070	100.0	2070	9	US-09-794-743-3	Sequence 3, Appli
4	2070	100.0	2070	9	US-09-794-748-3	Sequence 3, Appli
5	2070	100.0	2070	9	US-09-794-925-3	Sequence 3, Appli
6	2070	100.0	2070	9	US-09-681-442-3	Sequence 3, Appli
7	2070	100.0	2070	11	US-09-869-414-3	Sequence 3, Appli
8	2070	100.0	2070	11	US-09-548-366-3	Sequence 3, Appli
9	2032	98.2	2541	11	US-09-969-671A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-09-794-927-3

; Sequence 3, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

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; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-3

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Query Match          100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	 GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 2

US-09-795-847-3

; Sequence 3, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-795-847-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

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          |||
Db      1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 3

US-09-794-743-3

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; Sequence 3, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-743-3

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Query Match          100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960

Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800


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Qy      1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 4

US-09-794-748-3

; Sequence 3, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-748-3

Query Match

100.0%; Score 2070; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
      |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      |||
Db    301 GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
      |||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
      |||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Db    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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 Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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 Db 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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 Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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 Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
 Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG 1320
 Qy 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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 Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
 Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440
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 Db 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440
 Qy 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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 Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
 Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC 1620
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 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC 1620
 Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
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 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
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 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 2070
 ||||||||||||||||||||||||||||||||
 Db 2041 ATTAaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 2070

RESULT 5

US-09-794-925-3

; Sequence 3, Application US/09794925
 ; Patent No. US20020064819A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 28341/6280HI
 ; CURRENT APPLICATION NUMBER: US/09/794,925
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-925-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCGCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGCGCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA 300
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Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT 480
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Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
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Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
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Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
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Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560

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 |||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
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 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
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 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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 Db 1801 TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

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Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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RESULT 6

US-09-681-442-3

; Sequence 3, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-681-442-3
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Query Match          100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
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Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
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Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db 601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

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Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

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Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

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Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT 1800
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 7

US-09-869-414-3

; Sequence 3, Application US/09869414

; Publication No. US20030077226A1

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380

Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 8

US-09-548-366-3

; Sequence 3, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

```

; APPLICANT:  Heinrikson, Robert L.
; APPLICANT:  Parodi, Luis A.
; APPLICANT:  Yan, Riqiang
; TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION:  USES THEREFOR
; FILE REFERENCE:  28341/6280A
; CURRENT APPLICATION NUMBER:  US/09/548,366
; CURRENT FILING DATE:  2000-04-12
; PRIOR APPLICATION NUMBER:  60/155,493
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  09/404,133
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  PCT/US99/20881
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  60/101,594
; PRIOR FILING DATE:  1998-09-24
; NUMBER OF SEQ ID NOS:  65
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-366-3

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Query Match          100.0%; Score 2070; DB 11; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
        |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

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Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320

Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	 GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

US-09-969-671A-1
; Sequence 1, Application US/09969671A
; Publication No. US20030036112A1
; GENERAL INFORMATION:
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: MURPHY, KAY
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SMITH, TRUDI S.
; TITLE OF INVENTION: ASP2
; FILE REFERENCE: GH-70368-D1
; CURRENT APPLICATION NUMBER: US/09/969,671A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: UK 9701684.4
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 09/694,200
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unknown
; LOCATION: (2455) (2456) (2463) (2478) (2480) (2497) (2507) (2509) (2512) (2516)
; LOCATION: (2520) (2522) (2525) (2529) (2539) (2540)
; OTHER INFORMATION: Wherein n can be represented by a, c, t, or g
US-09-969-671A-1

Query Match 98.2%; Score 2032; DB 11; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Qy	61	GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360

Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200

Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTTC	1559
Db	1501	AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1619
Db	1561	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACC	1799
Db	1741	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1859
Db	1801	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1919
Db	1861	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979
Db	1921	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1980
Qy	1980	TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG	2039
Db	1981	TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG	2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059
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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 10

US-10-308-365-1

; Sequence 1, Application US/10308365
; Publication No. US20030109022A1
; GENERAL INFORMATION:
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: MURPHY, KAY
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SMITH, TRUDI S.
; TITLE OF INVENTION: ASP 2
; FILE REFERENCE: GH-70368-2
; CURRENT APPLICATION NUMBER: US/10/308,365
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/694,200
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: UK 9701684.4
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE: FEATURE: MISCELLANEOUS FEATURE
; NAME/KEY: UNSURE
; LOCATION: (2455) (2456) (2463) (2478) (2480) (2497) (2507) (2509) (2512) (2516) (2520)
; LOCATION: (2522) (2525) (2529) (2539) (2540)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t
US-10-308-365-1

Query Match 98.2%; Score 2032; DB 15; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
| | | | | | | | | | | | | | | | | |
Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
| | | | | | | | | | | | | | | | | |
Db 61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180
| | | | | | | | | | | | | | | | | |
Db 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180

Qy 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
| | | | | | | | | | | | | | | | | |
Db 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTTC	1559
Db	1501	 AAGTGAGGAGGCCCATGGGAGAAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTC	1619
Db	1561	 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1799
Db	1741	 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA	1859
Db	1801	 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA	1919
Db	1861	 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGGAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979

Db 1921 GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTGCTAT 1980

Qy 1980 TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
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Db 1981 TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059
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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 11

US-09-796-264-1

; Sequence 1, Application US/09796264
 ; Patent No. US20020049303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.
 ; APPLICANT: Lin, Xinli
 ; APPLICANT: Koelsch, Gerald
 ; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
 ; TITLE OF INVENTION: of Use Thereof
 ; FILE REFERENCE: OMRF 179
 ; CURRENT APPLICATION NUMBER: US/09/796,264
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/604,608
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-796-264-1

Query Match 97.1%; Score 2010; DB 9; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
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Db 1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy 100 CTGGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
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Db 61 CTGGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120

Qy 160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
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Db 121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCACCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCACCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAACCTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCGTGACGACTCC	579
Db	481	TCCAACCTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCGTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1959

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Db      1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy      1960 GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db      1921 GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 12

US-09-845-226-1

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; Sequence 1, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRP 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-226-1

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Query Match          97.1%; Score 2010; DB 10; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
Db      1  GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy     100 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
Db      61 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120

Qy     160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
Db     121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

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Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959

Db 121 CCCGGCCGGAGGGGAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180
 Qy 220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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 Db 181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 240
 Qy 280 ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 339
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 Db 241 ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 300
 Qy 340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360
 Qy 400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 459
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 420
 Qy 460 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
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 Db 421 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480
 Qy 520 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540
 Qy 580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
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 Db 541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600
 Qy 640 CACCTTTGTGGTGTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG 699
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 Db 601 CAGCTTTGTGGTGTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG 660
 Qy 700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720
 Qy 760 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780
 Qy 820 CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC 879
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC 840
 Qy 880 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
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 Db 841 AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900
 Qy 940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
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 Db 901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960
 Qy 1000 GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
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 Db 961 GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860

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Qy      1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 1959
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Db      1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAAACAAGCCTAACATT 2019
          |||
Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAAACAAGCCTAACATT 1980

Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
          |||
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 14

US-10-032-818-1

; Sequence 1, Application US/10032818

; Publication No. US20030092629A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Jordan J.N.

; APPLICANT: Koelsch, Gerald

; APPLICANT: Ghosh, Arun K.

; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof

; FILE REFERENCE: 2932.1006-007

; CURRENT APPLICATION NUMBER: US/10/032,818

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: US 60/275,756

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: US 60/258,705

; PRIOR FILING DATE: 2000-12-28

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3252

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-032-818-1

Query Match 97.1%; Score 2010; DB 15; Length 3252;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
          |||
Db      1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy      100 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
          |||
Db      61 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy      160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
          |||
Db      121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy      220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
          |||
Db      181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

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Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAACATTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179

Db	1081	 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTCA GTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	 TGCCTCATGGTGTGTCA GTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	 CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGCGGTGTGTCCC	1899
Db	1801	 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGCGGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861	 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1920
Qy	1960	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATT	2019

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Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAAAAAAAA 2057
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Db      1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAACACTAGA 2018

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RESULT 15

US-09-794-927-5

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; Sequence 5, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-5

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Query Match          91.2%; Score 1887.2; DB 9; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

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Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945

Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1785
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

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Db    1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845
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Qy    1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
      |||
Db    1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905
      |||
Qy    1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
      |||
Db    1906 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965
      |||
Qy    2041 ATTAAAAAAAAA 2052
      | |||
Db    1966 AAAAAAAAAA 1977

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